



003300-883.ST25

10 Rec'd PCT/PTC 21 MAR 2003  
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## SEQUENCE LISTING

&lt;110&gt; Leif, Leif

&lt;120&gt; RECOMBINANT ADENOVIRUS

&lt;130&gt; 003300-883

&lt;140&gt; US 10/019,566

&lt;141&gt; 2002-03-28

&lt;150&gt; SE 9902601-5

&lt;151&gt; 1999-07-06

&lt;150&gt; US 60/143,632

&lt;151&gt; 1999-07-14

&lt;150&gt; PCT/SE00/01390

&lt;151&gt; 2000-06-30

&lt;160&gt; 16

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 36

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;300&gt;

&lt;301&gt; Hoppe HJ, Barlow PN, Reid KBM

<302> A parallel three stranded  $\alpha$ -helical bundle at the nucleation site of collagen triple-helix formation

&lt;303&gt; FEBS Letters

&lt;304&gt; 344

&lt;306&gt; 191-195

&lt;307&gt; 1994

&lt;400&gt; 1

Pro Asp Val Ala Ser Leu Arg Gln Gln Val Glu Asp Leu Gln Gly Gln  
1 5 10 15Val Gln His Leu Gln Ala Ala Phe Ser Gln Tyr Lys Lys Val Glu Leu  
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Phe Pro Asn Gly

35

&lt;210&gt; 2

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;300&gt;

&lt;301&gt; Harbury PB, Zhang T, Kim PS, Albert T

&lt;302&gt; A switch between two-, three-, and four-stranded coiled coils in GCN4 leucine zipper mutants

&lt;303&gt; Science

&lt;304&gt; 262

<306> 1401-1407  
<307> 1993-11-26

<400> 2  
Met Lys Gln Ile Gly Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr  
1 5 10 15  
His Ile Glu Asn Gly Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu  
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<210> 3  
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<213> Pseudomonas aeruginosa

<300>  
<301> Brinkmann U, Buchner J, Pastan I  
<302> Independent domain folding of Pseudomonas exotoxin and single  
chain immunotoxins: Influence of interdomain connections  
<303> Proc. Natl. Acad. Sci. US  
<304> 89  
<306> 3075-3079  
<307> 1992

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Ala Ser Gly Gly Pro Glu  
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<300>  
<301> Brinkmann U, Buchner J, Pastan I  
<302> Independent domain folding of Pseudomonas exotoxin and single  
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<303> Proc. Natl. Acad. Sci. US  
<304> 89  
<306> 3075-3079  
<307> 1992

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<302> Independent domain folding of Pseudomonas exotoxin and single  
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<303> Proc. Natl. Acad. Sci. US  
<304> 89

<306> 3075-3079  
<307> 1992

<400> 5  
Ala Ser Thr Pro Glu Pro Asp Pro  
1 5

<210> 6  
<211> 13  
<212> PRT  
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Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ser Asp  
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<212> PRT  
<213> Homo sapiens

<300>  
<301> Dangl JL, Wensel TG, Morrison SL, Streyer L, Herzenberg LA,  
and Oi T  
<302> Segmental flexibility and complement fixation of genetically  
engineered chimeric human, rabbit and mouse antibodies  
<303> EMBO Journal  
<304> 7  
<306> 1989  
<307> 1988

<400> 7  
Thr Pro Leu Gly Asp Thr Thr His Thr Ser Gly  
1 5 10

<210> 8  
<211> 11  
<212> PRT  
<213> Adenovirus type 5

<300>  
<301> Stouten PFW, Sander C, Ruigrok WH, Cusack S  
<302> New triple-helical model for the shaft of the adenovirus fibre  
<303> Journal of molecular biology  
<304> 226  
<306> 1073-1084  
<307> 1992

<400> 8  
Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
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<210> 9  
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<212> PRT

<213> Simian virus 40

<300>

<301> Fisher-Fantuzzi L and Vesco C

<302> Cell-Dependent Efficiency of Reiterated Nuclear Signals in a  
Mutant Simian Virus 40 Oncoprotein Targeted to the Nucleus

<303> Molecular Cell Biology

<304> 8

<306> 5495-5503

<307> 1992

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Asp Pro Lys Lys Lys Arg Lys Val  
1 5

<210> 10

<211> 116

<212> PRT

<213> Homo sapiens

<400> 10

Gln	Lys	Val	Thr	Gln	Ala	Gln	Thr	Glu	Ile	Ser	Val	Val	Glu	Lys	Glu
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Asp	Val	Thr	Leu	Asp	Cys	Val	Tyr	Glu	Thr	Arg	Asp	Thr	Thr	Tyr	Tyr
			20				25						30		
Leu	Phe	Trp	Tyr	Lys	Gln	Pro	Pro	Ser	Gly	Glu	Leu	Phe	Leu	Ile	
	35					40					45				
Arg	Arg	Asn	Ser	Phe	Asp	Glu	Gln	Asn	Glu	Ile	Ser	Gly	Arg	Tyr	Ser
	50				55					60					
Trp	Asn	Phe	Gln	Lys	Ser	Thr	Ser	Ser	Phe	Asn	Phe	Thr	Ile	Thr	Ala
	65				70				75				80		
Ser	Gln	Val	Val	Asp	Ser	Ala	Val	Tyr	Phe	Cys	Ala	Leu	Gly	Gly	Val
		85				90					95				
Asn	Asn	Asn	Ala	Gly	Asn	Met	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Arg	Leu
			100			105						110			
Met	Val	Lys	Pro												
		115													

<210> 11

<211> 133

<212> PRT

<213> Homo sapiens

<400> 11

Glu	Asp	Leu	Asn	Lys	Val	Phe	Pro	Pro	Glu	Val	Ala	Val	Phe	Glu	Pro
1				5				10					15		
Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	Leu	Val	Cys	Leu
				20				25					30		
Ala	Thr	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Lys	Ser	Trp	Trp	Val	Asn
	35				40			45							
Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro	Gln	Pro	Leu	Lys
	50				55			60							
Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu	Ser	Ser	Arg	Leu
	65			70				75					80		
Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	His	Phe	Arg	Cys
		85			90						95				
Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	Thr	Gln	Asp

<210> 12  
<211> 113  
<212> PRT  
<213> *Homo sapiens*

<400> 12  
 Asp Ser Gly Val Thr Gln Thr Pro Lys His Leu Ile Thr Ala Thr Gly  
 1 5 10 15  
 Gln Arg Val Thr Leu Arg Cys Ser Pro Arg Ser Gly Asp Leu Ser Val  
 20 25 30  
 Tyr Trp Tyr Gln Gln Ser Leu Asp Gln Gly Leu Gln Phe Leu Ile His  
 35 40 45  
 Tyr Tyr Asn Gly Glu Glu Arg Ala Lys Gly Asn Ile Leu Glu Arg Phe  
 50 55 60  
 Ser Ala Gln Gln Phe Pro Asp Leu His Ser Glu Leu Asn Leu Ser Ser  
 65 70 75 80  
 Leu Glu Leu Gly Asp Ser Ala Leu Val Phe Cys Ala Ser Asn Ile Ala  
 85 90 95  
 Gly Gly Ser Tyr Thr Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr Val  
 100 105 110  
 Leu

```
<210> 13
<211> 53
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Sequence replacing the fiber gene sequence which was deleted between the NdeI restriction site in the fiber tail and the MunI site which begins at base 38 after the stop codon in the fiber. The sequence restores the NdeI and MunI sites and the wild type genome sequence between the fiber stop codon and the MunI site. In addition the added sequence contains an XhoI site allowing for the ligation of recombinant fibers.

<400> 13 tatgcactcg agtaaaagaat cgtttgtgtt atgtttcaac gtgtttattt ttc 53

<210> 14  
<211> 1746  
<212> DNA  
<213> Human adenovirus type 5

<220>  
<221> CDS  
<222> (1)...(1746)  
<223> 1-129 Fiber tail  
130-1200 Fiber shaft

## 1201-1746 Fiber knob

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 atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca 48  
 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro  
 1 5 10 15

5 10 15

96  
 tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc  
 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro  
 20 25 30

144  
 ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct  
 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
 35 40 45

192  
 ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc  
 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu  
 50 55 60

240  
 aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc  
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
 65 70 75 80

288  
 caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac  
 Gln Asn Val Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
 85 90 95

336  
 ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta  
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
 100 105 110

384  
 act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc  
 Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
 115 120 125

432  
 atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att  
 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
 130 135 140

480  
 gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa  
 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
 145 150 155 160

528  
 aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act  
 Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
 165 170 175

576  
 gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg  
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
 180 185 190

624  
 aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg  
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly  
 195 200 205

672  
 gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act  
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
 210 215 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act		720
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr		
225	230	235
240		
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca		768
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala		
245	250	255
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt		816
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val		
260	265	270
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag		864
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln		
275	280	285
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac		912
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn		
290	295	300
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag		960
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu		
305	310	315
320		
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata		1008
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile		
325	330	335
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca		1056
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro		
340	345	350
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat		1104
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp		
355	360	365
tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac		1152
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp		
370	375	380
agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act		1200
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr		
385	390	395
400		
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag		1248
Leu Trp Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu		
405	410	415
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata		1296
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile		
420	425	430
435		
ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata		1344
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile		
440		445
tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat		1392
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn		
450	455	460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt	1440
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe	
465 470 475 480	
aga aat gga gat ctt act gaa ggc aca gcc tat aca aac ggt gtt gga	1488
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Gly Val Gly	
485 490 495	
ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc	1536
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala	
500 505 510	
aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa	1584
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys	
515 520 525	
cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac	1632
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp	
530 535 540	
aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc	1680
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly	
545 550 555 560	
cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca	1728
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565 570 575	
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580	

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 35 40 45  
 Ala Ala Ile Asn Ser Asp Gly Gly Ile Thr Tyr Tyr Leu Asp Thr Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu Phe Tyr Cys  
 85 90 95  
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 115 120

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35 40 45  
Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly  
50 55 60  
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser  
65 70 75 80  
Glu Asp Leu Ala Asp Phe Phe Cys Gln Gln Tyr Ser Asn Tyr Pro Trp  
85 90 95  
Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala  
100 105 110  
Pro Thr Val Ser  
115